

Morris\_Supplementary\_Table\_1

Characteristics of dams mated with HFD and control males			
Group	control (n = 8)	HFD (n = 9)	P
BW (g)	291 ± 5	286 ± 6	0.53
Mesenteric WAT (g)	2.29 ± 0.17	2.20 ± 0.16	0.73
Retroperitoneal WAT (g)	3.06 ± 0.20	3.02 ± 0.43	0.93
Gonadal WAT (g)	2.16 ± 0.21	2.29 ± 0.28	0.71
Sum of WAT (g)	7.62 ± 0.53	7.51 ± 0.82	0.92
Glucose (mM)	4.13 ± 0.06	4.27 ± 0.09	0.21
Insulin (ng.ml <sup>-1</sup> )	0.08 ± 0.02	0.08 ± 0.01	0.93
HOMA-IR	0.34 ± 0.07	0.34 ± 0.06	0.98

HFD, high fat diet. BW, body weight. WAT, white adipose tissue. Sum of WAT, sum of mesenteric, retroperitoneal and gonadal WAT. All results are expressed as mean ± s.e.m.

Morris\_Supplementary\_Table\_2

Summary of differentially expressed genes in islets of female offspring of HFD vs control fathers (P&lt;0.001)

Gene Symbol	RefSeq	Probeset ID	Mean		HFD vs. control		GO biological process	GO cellular component	GO molecular function	
			HFD a (n=5)	control a (n=6)	Fold-change b	P value				
up-regulated										
LOC881708	ENSRNOT0000061706	1073343	5.46	4.96	1.42	6.66E-04	—	—	ENSRNOT0000061706 / GO:000166 / nucleotide binding / inferred from electronic annotation	
Mut4	ENSRNOT0000010596	1035418	6.67	6.36	1.24	8.52E-04	ENSRNOT0000010596 / GO:000468 / protein amino acid phosphorylation / inferred from electronic annotation	—	ENSRNOT0000010596 / GO:000287 / magnesium ion binding / not recorded / ENSRNOT0000010596	
LOC168242	NM_00109164	1072930	3.36	3.11	1.19	1.40E-04	—	—	—	
TubA3	NM_130254	1008702	7.73	7.49	1.18	2.78E-04	NM_130254 / GO:0007017 / microtubule-based process / inferred from electronic annotation	NM_130254 / GO:000822 / intracellular / inferred from electronic annotation / NM_130254	NM_130254 / GO:000166 / nucleotide binding / inferred from electronic annotation / NM_130254	
Fam188b	NM_001134633	1008711	4.83	4.39	1.18	9.51E-05	—	NM_001134633 / GO:004234 / protein complex / not recorded / ENSRNOT0000005472 / GO:004234	—	
—	—	1002026	8.50	8.28	1.17	1.05E-04	—	—	—	
LOC102624	NM_001092674	1007073	7.05	6.83	1.17	8.05E-04	—	—	—	
MGC12612	NM_001092638	1007170	7.33	7.11	1.16	4.25E-04	NM_001092638 / GO:0006330 / transcription / inferred from electronic annotation / NM_001092638	NM_001092638 / GO:000523 / intracellular / inferred from electronic annotation / NM_001092638	NM_001092638 / GO:000376 / nucleic acid binding / inferred from electronic annotation	
Slc3a5	NM_138854	1003699	11.75	11.56	1.14	5.23E-04	NM_138854 / GO:001954 / neutral amino acid transport / inferred from direct assay / NM_138854	—	NM_138854 / GO:0010171 / amino acid transmembrane transporter activity	
Bimk	NM_001024163	1074546	6.96	6.78	1.13	8.87E-04	NM_001024163 / GO:0006308 / proteolysis / inferred from electronic annotation / NM_001024163	NM_001024163 / GO:000525 / soluble fraction / not recorded / ENSRNOT0000005125 / GO:000625	NM_001024163 / GO:0004197 / cysteine-type endopeptidase activity / inferred from electronic annotation	
Vtic16	NM_001008911	10610818	2.96	2.78	1.13	7.94E-04	NM_001008911 / GO:0007186 / G-protein coupled receptor protein signaling pathway	NM_001008911 / GO:0016021 / integral to membrane / inferred from electronic annotation	NM_001008911 / GO:0004872 / receptor activity / inferred from electronic annotation	
Htt161	NM_181627	1071649	7.49	7.31	1.13	5.71E-04	—	NM_181627 / GO:0005624 / membrane fraction / inferred from direct assay	NM_181627 / GO:0005015 / protein binding / inferred from physical interaction / AY291962	
Cd321	ENSRNOT0000023274	1007480	6.98	6.82	1.12	1.80E-04	ENSRNOT0000023274 / GO:000468 / protein amino acid phosphorylation / inferred from electronic annotation	ENSRNOT0000023274 / GO:0005634 / nucleus / inferred from electronic annotation	ENSRNOT0000023274 / GO:000166 / nucleotide binding / inferred from electronic annotation	
—	—	10716742	5.26	5.11	1.12	8.99E-04	—	—	—	
Ohv57	NM_001000689	10637512	2.88	2.42	1.11	1.97E-04	NM_001000689 / GO:0007186 / G-protein coupled receptor protein signaling pathway	NM_001000689 / GO:0016021 / integral to membrane / inferred from electronic annotation	NM_001000689 / GO:0004984 / olfactory receptor activity / inferred from electronic annotation	
LOC1683986	QSOX3251	1066210	8.40	8.26	1.11	7.26E-04	—	—	—	
—	—	10682571	8.46	8.33	1.09	7.31E-05	—	—	—	
Spat	NM_001108702	1008879	8.06	7.93	1.09	6.49E-05	NM_001108702 / GO:0001578 / microtubule bundle formation	NM_001108702 / GO:0005634 / nucleus / inferred from sequence or structural similarity	NM_001108702 / GO:0000166 / nucleotide binding / inferred from electronic annotation	
Cxv1	ENSRNOT0000011865	1073775	8.14	8.05	1.07	4.52E-04	ENSRNOT0000011865 / GO:0006333 / chromatin assembly or disassembly	ENSRNOT0000011865 / GO:000775 / chromosome, centromeric region / not recorded	ENSRNOT0000011865 / GO:0003682 / chromatin binding / inferred from electronic annotation	
Tot1	NM_001025735	1071953	9.80	9.81	1.07	3.26E-04	NM_001025735 / GO:0005634 / RNA elongation / inferred from electronic annotation / NM_001025735	NM_001025735 / GO:0003677 / RNA binding / inferred from electronic annotation / NM_001025735	NM_001025735 / GO:0003677 / RNA binding / inferred from electronic annotation / NM_001025735	
Cxv3	NM_001008313	1061635	9.51	9.44	1.05	4.11E-05	NM_001008313 / GO:0006333 / chromatin assembly or disassembly / inferred from electronic annotation	NM_001008313 / GO:0000785 / chromatin / inferred from electronic annotation / NM_001008313	NM_001008313 / GO:0003682 / chromatin binding / inferred from electronic annotation	
down-regulated										
Dock5	NM_001114621	1083824	5.37	5.94	-1.48	2.39E-04	NM_001114621 / GO:0007242 / intracellular signaling cascade / inferred from electronic annotation	—	—	
LOC162863	XR_008675	10071081	4.13	4.64	-1.43	4.00E-04	—	—	—	
Emf4p	NM_001007588	10030717	3.75	4.17	-1.34	5.66E-04	NM_001007588 / GO:0007218 / neurotransmitter signaling pathway / inferred from electronic annotation	NM_001007588 / GO:000886 / plasma membrane / inferred from electronic annotation	NM_001007588 / GO:0004930 / G-protein coupled receptor activity / inferred from electronic annotation	
Car7	NM_001106165	10083007	4.44	4.84	-1.32	8.11E-04	NM_001106165 / GO:0006730 / one-carbon metabolic process / inferred from electronic annotation	—	NM_001106165 / GO:0004989 / carbonate dehydratase activity / inferred from electronic annotation	
LOC26521	NM_001008879	10053962	4.48	4.86	-1.30	5.90E-04	—	—	—	
Znf56	ENSRNOT00000003296	1003998	5.61	5.94	-1.25	4.69E-04	—	—	—	
—	—	10739686	7.25	7.58	-1.25	2.79E-04	—	—	—	
Pgap1	NM_001135164	1072799	6.41	6.24	-1.26	7.25E-04	NM_001135164 / GO:0007185 / signal transduction / inferred from electronic annotation	NM_001135164 / GO:000886 / plasma membrane / inferred from electronic annotation	NM_001135164 / GO:000785 / prostaglandin / receptor activity / not recorded / NM_001135164	
LOC130798	NM_001144850	10077448	5.76	6.08	-1.25	6.01E-04	NM_001144850 / GO:0006329 / lipid metabolic process / inferred from electronic annotation	NM_001144850 / GO:0005194 / lysosome / inferred from electronic annotation	—	
—	—	10088019	6.60	6.91	-1.25	3.98E-04	—	—	—	
LOC168399	ENSRNOT0000011883	10714930	7.31	7.62	-1.24	6.23E-04	ENSRNOT0000011883 / GO:0006045 / glycine catabolic process / inferred from electronic annotation	ENSRNOT0000011883 / GO:0005739 / mitochondrion / inferred from electronic annotation	—	
Ohv57	NM_001000689	10637512	5.07	5.38	-1.24	4.76E-04	NM_001000689 / GO:0007186 / G-protein coupled receptor protein signaling pathway	NM_001000689 / GO:0016021 / integral to membrane / inferred from electronic annotation	NM_001000689 / GO:0004872 / receptor activity / inferred from electronic annotation	
LOC130824	NM_001134517	1064393	4.16	4.47	-1.24	6.37E-04	—	—	—	
—	—	1078220	1.91	2.20	-1.23	4.16E-04	—	—	—	
Cyp4a3	NM_175760	1008797	4.72	5.02	-1.23	6.01E-04	NM_175760 / GO:0001822 / kidney development / inferred from expression pattern / NM_175760	NM_175760 / GO:000570 / endoplasmic reticulum / inferred from electronic annotation	NM_175760 / GO:0008391 / arachidonic acid monooxygenase activity / inferred from mutant phenotype	
Atb1	NM_001109238	1008969	4.88	5.18	-1.23	4.32E-04	NM_001109238 / GO:0001764 / neuron migration / not recorded / NM_001109238 / GO:0008915	—	NM_001109238 / GO:0003677 / RNA binding / not recorded / NM_001109238 / GO:0008915	
Stp5a	NM_0211775	10015955	4.79	5.08	-1.23	1.73E-04	NM_0211775 / GO:0007185 / signal transduction / inferred from electronic annotation / NM_0211775	NM_0211775 / GO:000886 / plasma membrane / inferred from electronic annotation / NM_0211775	NM_0211775 / GO:0001619 / lysophosphatidyl and lysophosphatidic acid receptor activity	
Fu6b	ENSRNOT00000005941	10087398	6.17	6.47	-1.23	2.54E-04	—	ENSRNOT00000005941 / GO:0005634 / nucleus / not recorded / ENSRNOT00000005941 / GO:000537	—	
Fam132b	ENSRNOT0000001810	10025415	5.79	6.09	-1.23	3.04E-04	—	—	—	
LOC88899	ENSRNOT00000034362	10083332	6.15	6.44	-1.23	1.68E-04	—	—	—	
Wap2	NM_031590	10042043	5.92	6.21	-1.22	4.43E-05	NM_031590 / GO:0001598 / regulation of cell growth / inferred from electronic annotation	NM_031590 / GO:0005676 / extracellular region / inferred from electronic annotation / NM_031590	NM_031590 / GO:0005015 / protein binding / inferred from electronic annotation / NM_031590	
LOC1034737	ENSRNOT00000027883	10060279	6.47	6.76	-1.22	2.27E-04	ENSRNOT00000027883 / GO:0008955 / immune response / inferred from electronic annotation	ENSRNOT00000027883 / GO:0005622 / intracellular / inferred from electronic annotation	ENSRNOT00000027883 / GO:0003723 / RNA binding / inferred from electronic annotation	
Tnc2	NM_017185	10712471	4.85	5.13	-1.21	8.06E-04	NM_017185 / GO:0003009 / skeletal muscle contraction / not recorded / NM_017185 / GO:0006037	NM_017185 / GO:0005634 / nucleus / not recorded / NM_017185 / GO:000861 / tropomyosin complex	NM_017185 / GO:0003674 / molecular function / no biological data available / NM_017185	
—	—	10671483	6.81	6.48	-1.21	4.55E-05	—	—	—	
Neug1	NM_019207	10719599	5.30	5.57	-1.20	4.54E-04	NM_019207 / GO:0007275 / multicellular organismal development / inferred from electronic annotation	NM_019207 / GO:0005634 / nucleus / inferred from electronic annotation / ENSRNOT00000118916	NM_019207 / GO:0003677 / DNA binding / inferred from electronic annotation / NM_019207	
Itgq	NM_001014230	10711601	4.26	4.53	-1.20	7.36E-04	—	—	—	
—	—	10688794	2.57	2.83	-1.19	4.67E-04	—	—	—	
RSD1681557	NM_001108929	1062548	7.71	7.96	-1.19	9.14E-04	—	NM_001108955 / GO:0046905 / keratin filament / inferred from electronic annotation	NM_001108955 / GO:0005955 / electron carrier activity / inferred from electronic annotation	
—	—	10779427	4.90	5.15	-1.19	2.81E-04	—	—	—	
Scaat5	NM_001138655	1078131	5.90	6.15	-1.19	5.51E-04	NM_001138655 / GO:0008879 / cellular ion homeostasis / not recorded / NM_001138655	NM_001138655 / GO:000887 / integral to plasma membrane / not recorded / NM_001138655	NM_001138655 / GO:0003044 / scavenger receptor activity / inferred from electronic annotation	
Tgpl1	ENSRNOT00000002834	10710063	6.66	6.90	-1.18	5.57E-04	—	ENSRNOT00000002834 / GO:0005737 / cytoplasm / not recorded / ENSRNOT00000002834 / GO:000573	—	
Krtap4.7	ENSRNOT00000016879	10747162	6.89	7.13	-1.18	8.09E-04	—	—	—	
Nhe	NM_001109149	10723220	4.57	4.80	-1.18	2.13E-04	NM_001109149 / GO:0007204 / elevation of cytosolic calcium ion concentration	NM_001109149 / GO:0019171 / synapsome / inferred from direct assay / ENSRNOT00000014039	NM_001109149 / GO:0031710 / neurotransmitter B receptor binding / inferred from physical interaction	
RSD168166	NM_001016762	10737622	5.19	5.42	-1.17	9.62E-05	—	—	—	
Tgrrap3	NM_001047100	10060263	5.83	6.05	-1.17	1.04E-04	NM_001047100 / GO:0006508 / proteolysis / inferred from electronic annotation	NM_001047100 / GO:000886 / plasma membrane / inferred from electronic annotation	NM_001047100 / GO:0004252 / serine-type endopeptidase activity / inferred from electronic annotation	
—	—	10736596	7.10	7.32	-1.17	1.24E-04	—	—	—	
LOC279158	ENSRNOT00000006804	10064000	6.65	6.87	-1.16	7.33E-04	—	ENSRNOT00000006804 / GO:0005634 / nucleus / inferred from electronic annotation	ENSRNOT00000006804 / GO:0003677 / DNA binding / inferred from electronic annotation	
Abca10	NM_001108201	10071696	6.05	6.26	-1.16	3.92E-04	NM_001108201 / GO:0008190 / biological process / no biological data available	NM_001108201 / GO:0005737 / cellular component / no biological data available	NM_001108201 / GO:0003674 / molecular function / no biological data available	
—	—	10732272	4.52	4.73	-1.16	3.53E-04	—	—	—	
—	—	10071048	5.04	5.25	-1.16	4.51E-04	—	—	—	
Glyat1	NM_177936	10024298	5.64	5.85	-1.16	1.34E-04	NM_177936 / GO:0007185 / signal transduction / inferred from electronic annotation / NM_177936	NM_177936 / GO:000886 / plasma membrane / inferred from electronic annotation / NM_177936	NM_177936 / GO:0004872 / receptor activity / inferred from electronic annotation / NM_177936	
Upk3a	NM_001130507	10089291	5.82	6.02	-1.15	2.61E-04	NM_001130507 / GO:0009092 / cell morphogenesis / not recorded / NM_001130507 / GO:0001822	NM_001130507 / GO:0016234 / apical plasma membrane / not recorded / ENSRNOT00000014935	—	
—	—	10082841	9.78	9.98	-1.15	9.82E-04	—	—	—	
Whf6	NM_001070555	10748113	6.19	6.39	-1.15	8.16E-04	—	—	—	
LOC362626	NM_001025021	10060244	7.56	7.76	-1.15	3.74E-04	—	NM_001025021 / GO:0016020 / membrane / inferred from electronic annotation / NM_001025021	NM_001025021 / GO:0031072 / heat shock protein binding / inferred from electronic annotation	
Pcpln	NM_001008209	10089233	5.71	5.91	-1.15	8.34E-04	—	NM_001008209 / GO:0005604 / basement membrane / not recorded / ENSRNOT000000012757	—	
Ctr136	NM_001000160	10709458	4.76	4.95	-1.14	3.16E-04	NM_001000160 / GO:0007186 / G-protein coupled receptor protein signaling pathway	NM_001000160 / GO:0016021 / integral to membrane / inferred from electronic annotation	NM_001000160 / GO:0004984 / olfactory receptor activity / inferred from electronic annotation	
Ohp2	NM_001008851	10719508	4.94	5.12	-1.13	7.20E-04	—	—	—	
Slu2	NM_134457	10623338	7.94	8.12	-1.13	5.47E-04	NM_134457 / GO:0008511 / ubiquitin-dependent protein catabolic process / inferred from electronic annotation	NM_134457 / GO:0005624 / membrane fraction / inferred from direct assay / NM_134457	NM_134457 / GO:0004842 / ubiquitin-protein ligase activity / inferred from electronic annotation	
Sddp2	NM_001025682	10643750	4.74	4.92	-1.13	8.88E-04	—	NM_001025682 / GO:0005737 / cytoplasm / not recorded / ENSRNOT000000012890 / GO:000837	NM_001025682 / GO:0005015 / protein binding / inferred from electronic annotation / NM_001025682	
—	—	109114801	5.11	5.28	-1.13	7.09E-04	—	—	—	
—	—	10776577	4.29	4.46	-1.12	3.77E-04	—	—	—	
—	—	10763014	4.95	5.11	-1.12	2.30E-05	—	—	—	
Kb101	NM_001108170	10911745	3.80	3.96	-1.12	3.96E-04	—	—	—	
Gp162	NM_001108646	10605978	6.47	6.62	-1.11	5.94E-04	—	—	—	
Fam170a	NM_001126293									

HFD, high fat diet.

a Values represent fluorescent intensity of probe set and are presented in log 2 space.

b Fold change is gene expression of female offspring from HFD father relative to control.

Morris\_Supplementary\_Table\_3

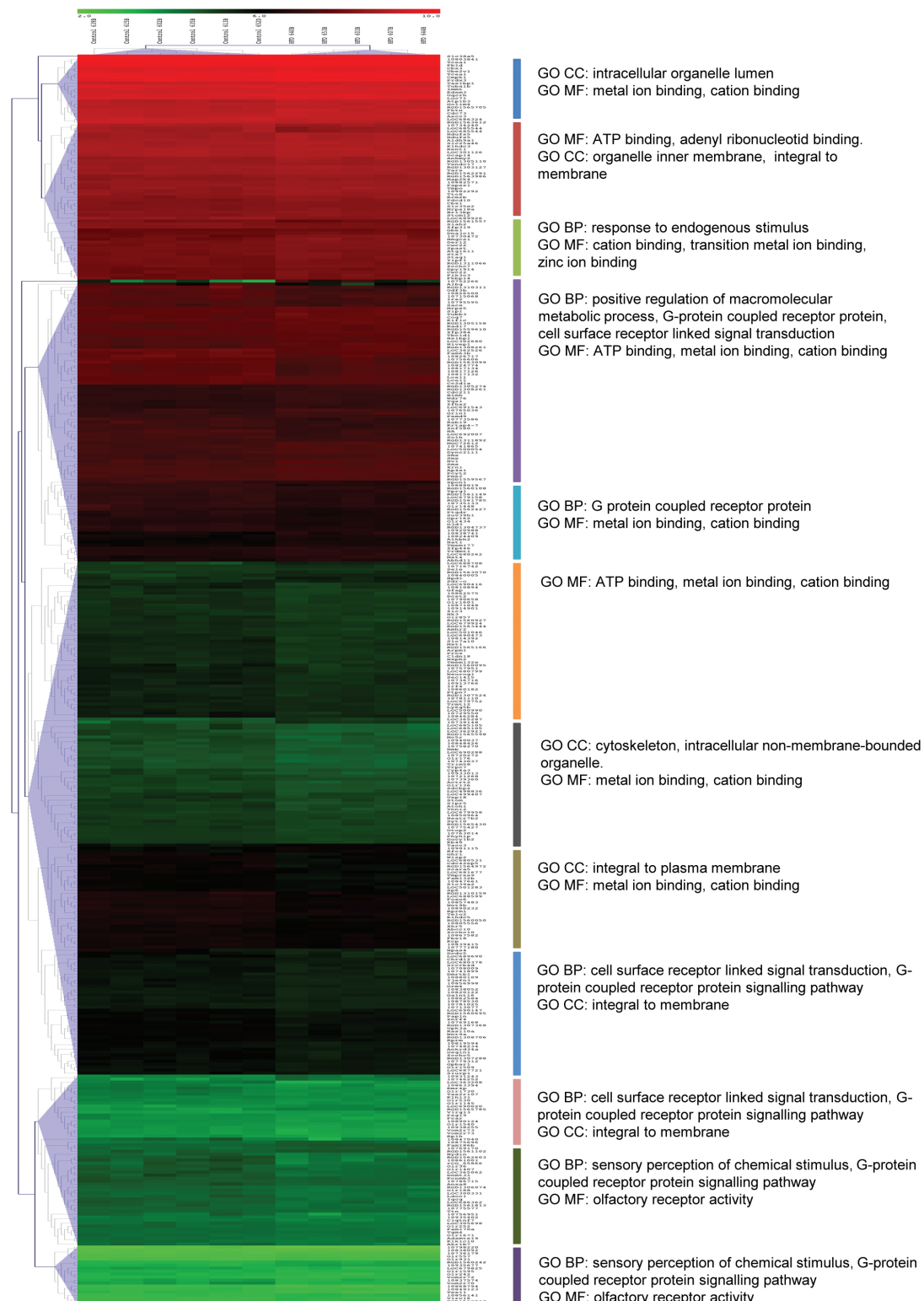
## Molecular networks of differentially expressed islet genes of female offspring

ID	Molecules in Networks generated from differentially expressed genes	Score	Focus Molecules	Top Functions
<b>Significance at <math>P &lt; 0.01</math></b>				
1	Ap1, CBX1, CBX3, CFL1, FCAR, Histone h3, Histone h4, HIVEP1, Iga, IL1, IL12 (complex), Interferon alpha, JAK, LDL, LY96, MPL, MST1, NEUROG1, NFkB (complex), OSGIN1, PTGDR, RARB, RPRM, SELE, SIAH2, STAT, STAT1, STAT5a/b, SUV39H1, TANK, TAX1BP1, TCEA1, TNFSF14, TXNDC17, USP18	32	23	Gene Expression, Cell-To-Cell Signaling and Interaction, Cellular Movement
2	AKR1B7, Akt, ATG16L1, Calmodulin, Caspase, DAP3, DUSP9, ERK, ERK1/2, FOXO6, FSH, GHRL, GRIN1, Hsp90, HTR7, Insulin, IRS2, Lh, MAP2K4, MAP3K4, NMB, P38 MAPK, PDCD10, P13-kinase, PIK3C3, Pkc(s), PP2A, PTPN7, RAB27A, RAD17, Ras, RFC4, RP6-213H19.1, TMPO, ZFP386	28	21	Behavior, Digestive System Development and Function, Organismal Development
3	26s Proteasome, Alp, Alpha tubulin, ASCL2, CDC42EP5, CHRD12, CXORF15, EGLN1, F Actin, FGD4, GDF5, GFAP, GTF2A1, HK3, HMGCS1, Immunoglobulin, IREB2, Jnk, KDM6A, KIF22, Mapk, NCOA6, Nfat (family), PDGF BB, PDGF-AA, PDLIM1, PODXL, POLH, SERTAD2, SLC29A1, TGS1, TRIB1, TTN, TUBA1B, TUBB3	21	17	Cell Cycle, Embryonic Development, Gene Expression
4	ATP1A3, ATXN1, C10RF106, C9ORF82, CFL1, CMPK1, CSE1L, DCTD, EXO1, FAM189A2, GFAP, HOXA5, HSPH1, KLC2, MSH6, PAPLN, PMS2, PSD2, PSME3, PTN, RFC4, SFN, SHC1, SNCAIP, STAG1, SUB1, TACC3, TP53, TP53BP2, TUBB3, WFDCC2, YWHAZ, ZCCHC10, ZHX2, ZHX3	21	17	DNA Replication, Recombination, and Repair, Nucleic Acid Metabolism, Small Molecule Biochemistry
5	ACVR1B, ADCYAP1, AMHR2, APP, ASCC1, ASCC3, CD68, CFL1, DLL3, GFAP, HMGB1 (includes EG:25459), IL10, INHBA, JUN, Kallikrein, KLK1, LHB, LINGO1, MMP1 (includes EG:4312), PODXL, POU1F1, PSG18, PSMD9, RTN4R, SFTPD, SP6, SPI1, SPIB, SPON1, TGM4, TNFRSF19, TRIP4, WDR90, WT1, ZNF384	19	16	Cell-To-Cell Signaling and Interaction, Free Radical Scavenging, Gene Expression
6	A1BG, C15ORF29, C10RF163, C20ORF4, DHRS7B, DYNC2LI1, EDEM3, EP300, FOXA2, FTSJ1, GH1, GOLIM4, GSK3B, HNF4A, Insulin, KLHDC3, LGALS3, MAP3K7, MYST2, NME1, NVL, ONECUT1, PBLD, PRKAB1, SHH, SLC2A4, SMAD3, SNRPD2, SNX5, STOML2, STRAP, TGFBI, TRAF6, TRMT12, UTP11L (includes EG:51118)	17	15	Gene Expression, Cellular Development, Connective Tissue Development and Function
7	AP2M1, CAMK2B, CCDC33, FAM190B, GFAP, HGS, HTT, KCNMA1, KCNMB3, KLHDC5, LDOC1, MTOR, NDUFS3, NDUFS5, NDUFV2, PFK, PFKP, RCN3, RHOBTB3, RPH3A, SDHB, STX1A, SYN2, SYT3, SYT6, TELO2, TNNI2, TPI1, TRDMT1, UBQLN1, VDACC3, ZBTB8A, ZIC3, ZNF250	16	14	Cell-To-Cell Signaling and Interaction, Nervous System Development and Function, Protein Trafficking
8	AKR1B7, AR, CHTF18, Ck2, CLDN3, CLDN4, CLDN5, CLDN6, CLDN7, CLDN8, CLDN18, DCTPP1, DIMT1L, EIF4E, ETV5, GJD3, GLCC1, KIF1C, LSM5, LSM6, LSM7, MC5R, MYC, NAP1L1, NKX2-1, OPRD1, OPRK1, POMC, PTPRT, PTRF, RRM2B, STAT3, TJP1, TMF1, WARS	16	14	Hematological Disease, Renal and Urological Disease, Endocrine System Development and Function
9	ALAS2, ARNT, ARNT2, ARNTL, BAT3, BMI1, CACNG1, CCT5, E2F4, EPAS1, EPO, EXOSC8, FAM173A, FLT1, HOXC5, IMMT, IQCC, IRS2, KIF22, LDHA, LIFR, MYOM2, NFE2, NPAS4, OMA1, RAB19, SLC2A1, SMARCD2, STAT5A, STX5, SUV39H1, TYROBP, WDR76, XRN1, ZFX2	14	13	Hematological Disease, Respiratory Disease, Gene Expression
10	ABHD5, ALB, AP4E1, APTX, BTG1, C14ORF1, C1QTNF7, CFB, ELL, F2, HMGB1 (includes EG:25459), HYLS1, LLP, NFIC, NR3C1, Nuclear factor 1, PEG3, PHYHIP, PLIN5, PNPLA2, PODXL, POLE2, PROZ, SERPING1, SGPL1, SPAST, STOM, TFAP4, THBD, TMED9, TP53, TRIO, TUBB3, ZNF446, ZNF24 (includes EG:7572)	14	13	Lipid Metabolism, Small Molecule Biochemistry, Cardiovascular Disease
<b>Significance at <math>P &lt; 0.05</math></b>				
1	AATK, BCKDHA, C/ebp, CEBPE, CENPJ, DAZAP1, FCAR, FOXE1, HK3, HPGD, IL13RA2, IRG1, KRT23, LRRC8C, LXN, PDPN, PDRG1, PEBP4, PHACTR3, PRG2, RAPGEF6, RASD1, RBP3, REC8, SCGB3A2, SERPIND1, SLC14A2, SMC1B, SSPO, TNF, TREM2, UBD, UGCG, UGT2B4, WTAP	36	34	Lipid Metabolism, Molecular Transport, Small Molecule Biochemistry

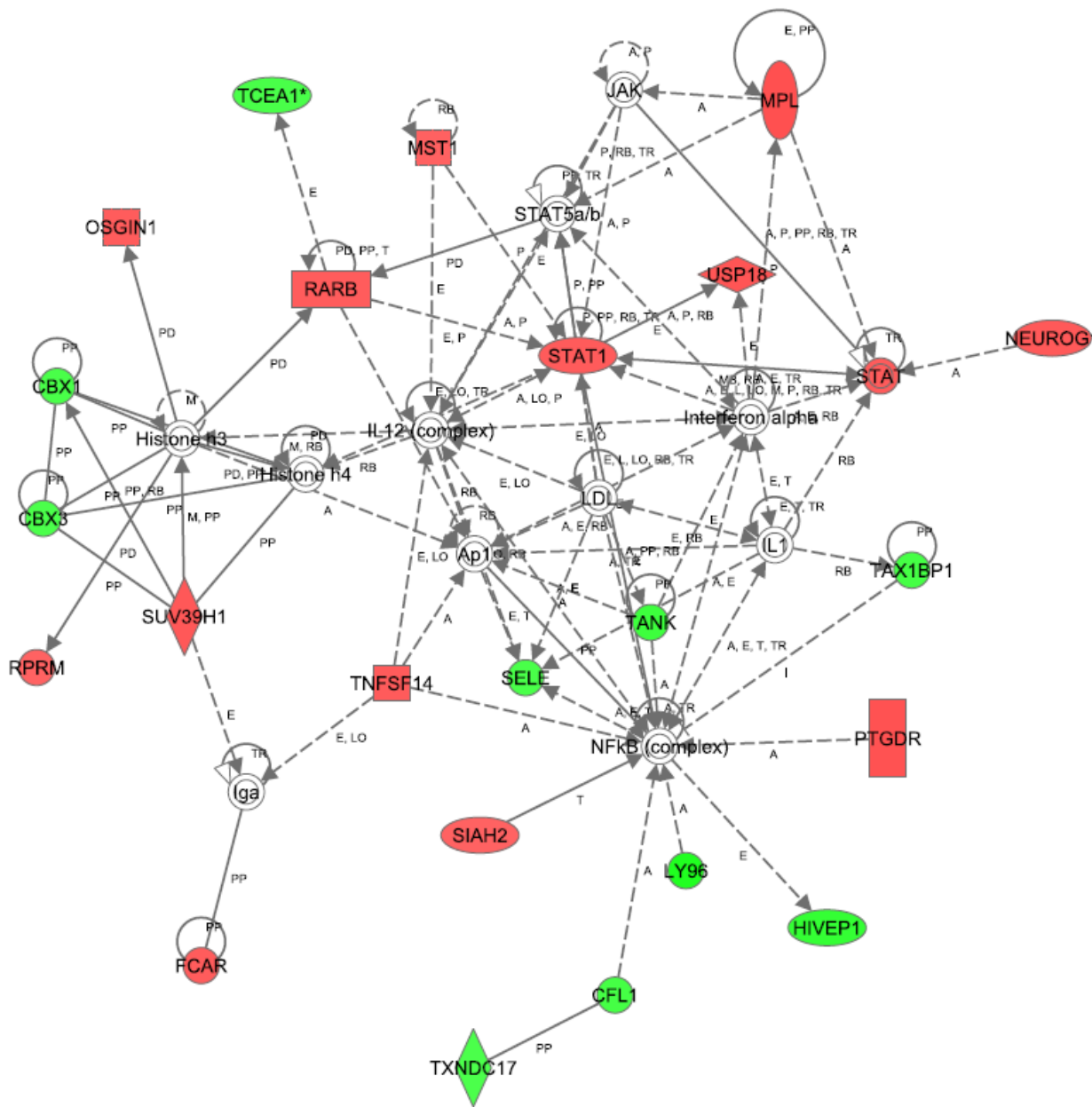
## Morris\_Supplementary\_Table\_4

## Primer sequences for RT-PCR

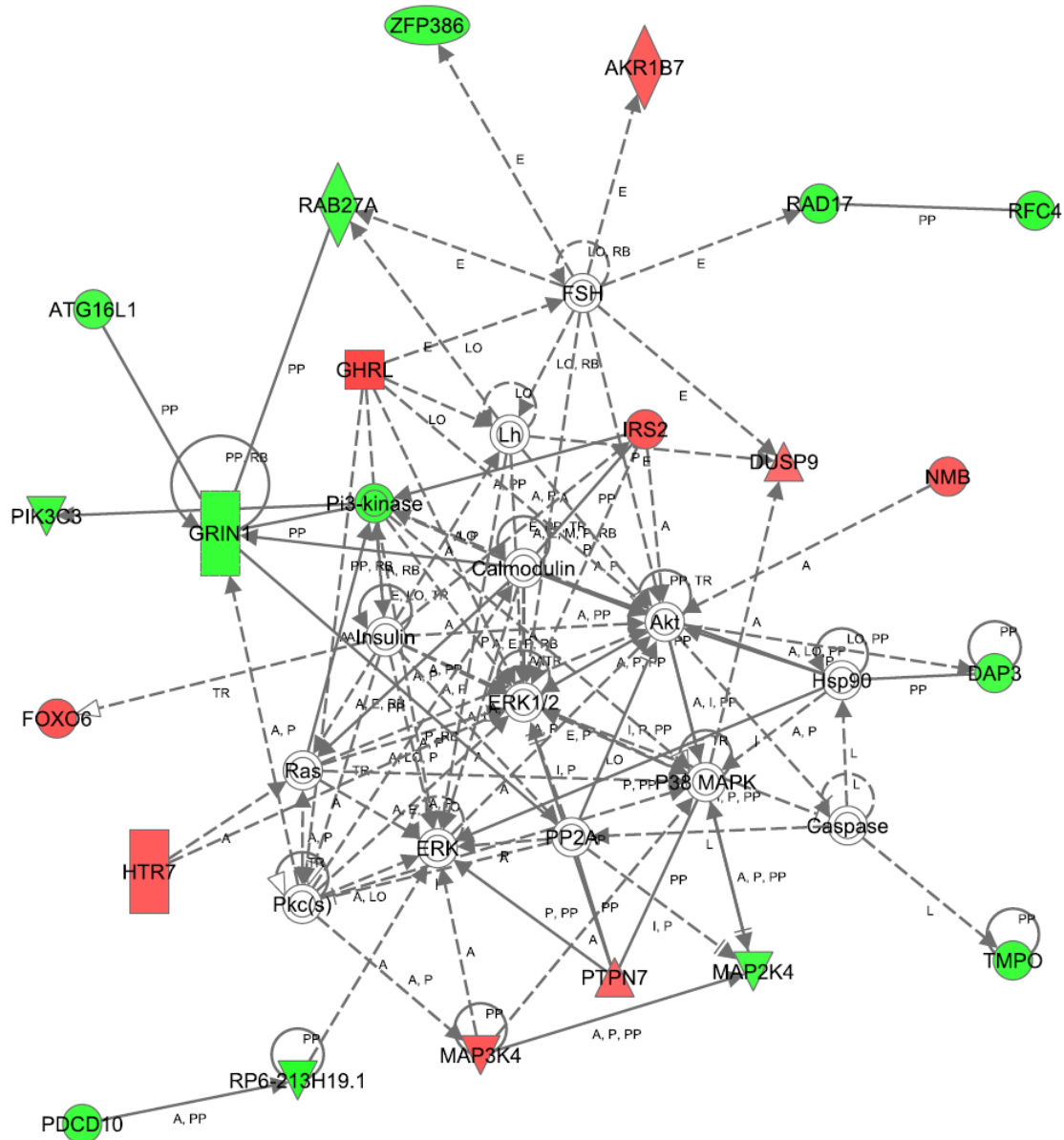
Gene symbol	Forward Primer (5'-3')	Reverse Primer (5'-3')
Il13ra2	CTTCCAGGCTAAAGCAGAATA	CTCTAGTTTCTGGAAGCACTCTG
Fos	AGCTCCCACCAAGTGTCTAC	GGCTGGGGAATGGTAGTAG
Ikbke	TGTACAAGGCCCGGAATA	CCTCCACTGCGAATAGCT
$\beta$ -actin	CACCCGCGAGTACAACCTTC	CCCATACCCACCATCACACC



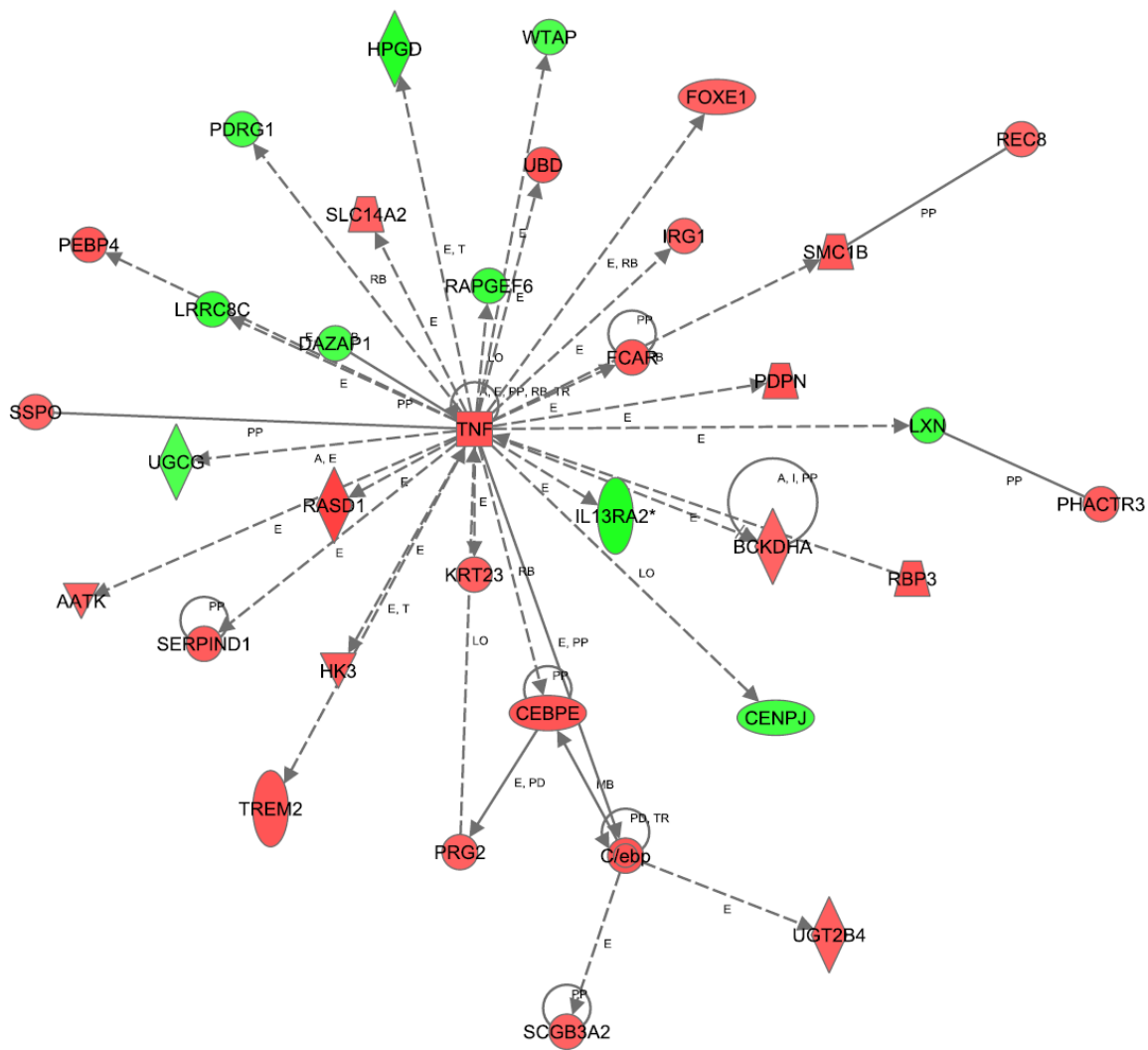
Supplementary Figure 1. Hierarchical clustering and functional annotation of differentially expressed islet genes ( $P < 0.01$ ) of HFD vs control offspring. Thirteen clusters were arbitrarily annotated and the most significant over-represented GO terms are described here. We observed an over-representation of genes belonging to cation and ATP binding, cytostructure and intracellular transport.



Supplementary Figure 2. Molecular Network 1 of differentially expressed islet genes in HFD female offspring,  $P < 0.01$  (Supplementary Table 3). This includes members of the enriched Jak-STAT signalling pathway. Molecules are represented as nodes, the biological relationship between two nodes is represented as an edge (line) and changed expression as up- (green) or down- (red) regulation.



Supplementary Figure 3. Molecular Network 2 of differentially expressed islet genes in HFD female offspring,  $P < 0.01$  (Supplementary Table 3). This includes members of the enriched MAPK signalling pathway and other molecules related to insulin action. Molecules are represented as nodes, the biological relationship as an edge (line) and changed expression as up- (green) or down- (red) regulation.



Supplementary Figure 4. Molecular Network 1 of differentially expressed islet genes of HFD female offspring,  $P < 0.05$  (Supplementary Table 3). This includes *tnf* (MAPK signalling and apoptosis pathways) and *Il13ra2* (Jak-STAT pathway), shown to be epigenetically modified by a paternal HFD. Molecules are represented as nodes, the biological relationship as an edge (line) and changed expression as up- (green) or down- (red) regulation.